7.84

```
Database: Issued_Patents_NA:*
Database sequences: 207703
Database length: 57918730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     About: Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM of: US-08-962-560A-4 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query length: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
Query: US-08-962-560A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters
                                                                                                                                 nl_6/ptcdata/2/ina/5A_COMB.seq:US-08-050-131 + 119.50 152.99 0.1177 2508 nl_6/ptcdata/2/ina/5A_COMB.seq:US-08-050-349A-1 + 119.50 159.90 0.1749 337 nl_6/ptcdata/2/ina/5A_COMB.seq:US-08-167-035-1 + 119.50 159.90 0.1749 337 nl_6/ptcdata/2/ina/5A_COMB.seq:US-08-208-87A-1 + 119.50 159.90 0.1749 337 nl_6/ptcdata/2/ina/5A_COMB.seq:US-08-87A-1 + 119.50 159.90 0.1749 337 nl_6/ptcdata/2/ina/5A_COMB.seq:US-08-059-05-1 + 119.50 159.90 0.1749 337 nl_6/ptcdata/2/ina/5A_COMB.seq:US-08-059-05-1 + 119.50 159.90 0.1749 337 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-059-08-27-1 + 116.50 128.59 9.70 131.74 6.47 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-08-27-1 + 116.50 128.59 9.70 131.74 6.47 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-08-27-1 + 119.50 159.90 0.1749 337 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-08-20-389-1 + 109.50 131.74 6.47 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-08-20-389-7 + 109.50 131.74 6.47 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-08-08-08-20-389-7 + 109.50 141.21 1.92 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-08-359A-5 - 104.00 119.78 30.03 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-853-659A-2 - 104.00 119.78 30.03 nl_6/ptcdata/2/ina/5B_COMB.seq:US-08-853-659A-3 - 104.00 114.92 55.96 nl_6/ptcdata/2/ina/5B_COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search time (sec): 62.100000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MODEL-frame+_P2n.model -DEV-xlp
-C-C-Cgn1_1/USFTO_spool/US08962560/runat_03022000_141755_3093/app_query.fasta.1
-DB-Issued_Patents_NA -QFMT-fastap -SUFFIX-rn1 -GAPOP-12.000
-GAPEXT-4.000 -MINAATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-7.000 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -STARTA1 - MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-PCT
-ALIGN-15 -MODE-LOCAL -OUTFMT-Pfs -NORM-ext -MINLEN-0
-MAXLEN-100000 -USER-US08962560 -NCFU-6 -ICFU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149.50
9.50
9.50
36
50
351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2e-13
                                                                                                                                                                                                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-265-310-1 +
/cgn1_6/ptodata/2/ina/5D_COMB.seq:US-08-318-837-1 -
/cgn1_6/ptodata/2/ina/5B_COMB.seq:US-08-310-691B-41
/cgn1_6/ptodata/2/ina/5B_COMB.seq:US-08-187-785-1 +
                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                     US-08-962-560A-4 x US-08-463-081B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                               14 SerProAlaAlaGluProArgArgArgSerGluProSerSerSerSerSe 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
rSerSerProAla...AlaProValArg...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9007
                                                                                                                                                                                                                                          .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                          US-08-463-081B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                      249.50
1.835
45.791
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-463-081B-9
                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1viana Amzel, Ph. D.
REGISTRATION NUMBER: US 03030
REFERENCE/DOCKET NUMBER: 966 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08463081B Patent No. 5871960 Patent No. 5871960 5837487
                                                                                                                                                                              TELEFAX: (213) 489-421
INFORMATION FOR SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 F
TITLE OF INVENTION: Vector and Transformed Cell
                                                                                                                STRANDEDNESS: single
                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Los Angeles
: California
                                                                                                                                                               1960 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: PRETTY, SCHROEDER & POPLAWSKI
444 South Flower St. - Suite 1900
CDS
112..886
                                                                                                 linear
                                                                        CDNA
                                                                                                                                                                                                                 ) 489-4210
ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .13
```

Percent

Gaps: : Identity:

297 10 27.946

from:

8

1960

OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Version #1.25 CURRENT APPLICATION NAME: APPLICATION NAME: FILING DATE: 5-UNE-1995 FRIOR APPLICATION NUMBER: USON 09/330,108; 08/104,736 APPLICATION NUMBER: USON 99/330,108; 08/104,736 APPLICATION NUMBER: USON 99/330,108; 08/104,709/300,009/300,	ENTION: Wester and T ENTION: Expression T EQUALITY OF THE STATE OF THE
--	--

Ξ

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-462-390B-9
                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                        845 GGCGCATGGCCGACTACCTCCGACAGTACCCCTTCCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 GlnArgArgValArgProLeuGlnGluLeuCysArg......GlnAr 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 gIleValAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 TGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGCTCCCACCCCGGC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                         199 roValLeuArgAspTyrLeuSerSerPheProPheGlnIle 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 CCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGACCCAGAGGAGGAT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 CATGCAGCCCTTGCCTGGGGGCCTTCCTCGAGGAGGTGGCAGAGGGTA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49
                                                                                                              ADDRESSEE:
                                                         COUNTRY:
                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tLeuGlyAlaPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eGlnAlaGlyArgPheHisLeuAspGly.....SerArgGlu.... 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHisPh 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGGTGGCCGACGTGGAC.....TGCCTGCCACTGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCACCAGCCACTGCTGTACACCTAAAACTGGTGCAGCCCTTTGTACGC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTGGCCTTTCCGGATGTGGTCAGCCTTGTGCAGCACTATGTGGCCTCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ThrPheAspCysLeuPheGluLeuLeuGluHisTyrValAla... 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGACTCCAGCTTCCGTCTGGACTCCAACTGCTTGTCCAGGCCACGCA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAAGGCACGTTCTTAGTACGTGACAGCACGCACCCCAGCTACCTGTTC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roValGlyThrPheLeuValArgAspSerArgGlnArgAsnCysPhePhe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGGGTTCCATTACGGCCAGCGAGGCCCGACAACACCTGCAGAAGATGC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGCTGTCAGTGAAAACCACTCGTGGCCCCACCAATGTACGCATTGAGTA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rTrpGlyProLeuSerValH1sGlyAlaH1sGluArgLeuArgAlaGluP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTy 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..ProAlaProGlyAspThrHisPheArgThrPheArgSerHisSerAsp
                                      19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....AlaProArgArgMe 162
                                                                                             Valley Forge
                                                                        Pennsylvania
Floppy disk
                                                                                                              (B
                                                                                                            STREET:One Westlakes-Berwyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....LeuArg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
```

```
alignment_block:
US-08-962-560A-4 x US-08-462-390B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-462-390B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-462-390B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (610)407-070 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                     260 CCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGACCCAGAGGAGGAT 309
                                                                                                                                                                                                                                                                160 ACTGGGCAGCGGCCCCTGTGGGCCCCGTCCCTGGAACTGCCCAAGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS LENGTH: 1960 base pai:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: USSN 07/796,066 FILING DATE: 20-NOV-91 ATTORNEY/AGENT INFORMATION:
                                                   210 CATGCAGCCCTTGCCTGCGGGCCTTCCTCGAGGAGGTGGCAGAGGGTA 259
                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 SerProAlaAlaGluProArgArgArgSerGluProSerSerSerSerSe::::||| ||| |||
49 ..ProAlaProGlyAspThrHisPheArgThrPheArgSerHisSerAsp
                                                                                                                                                                                                                                                                                                  46
                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                    65 TyrArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTy
                                                                                                                                                                                                                                                                                                                                                                                                                                      30 rSerSerProAla...AlaProValArg......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GCCCCGGGAGCCTACCCAGCACGCGCTCCGCGCCCACTGGTTCCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
                                                                                                                                                                                                                             ..... 48
                                                                                                                                                                                                                                                                                                                                                                  .....ProArgProCysProAlaVal..... 46
                                                                                                                                                                                                                                                                                                                                                                                                         CCGCCGCCGTCCAGCCGAGTCCCCACTCCGGAGTCGCCGCTGCCGCGGGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (610)407-0701
NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
112..886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249.50
1.835
45.791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/462,390B
                                                                                                                                                                                                                                                                                                  46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DART-040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
27.946
                                                                                    81
                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
```

```
seq_name: /cgnl_6/ptodata/2/ina/5D_COMB.seq:US-08-918-206-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
CURRENT APPLICATION NUMBER: US/08/918,206
FILING DATE: Flied Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/918,206
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08918206 Patent No. 5919661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 .....ThrPheAspCysLeuPheGluLeuLeuGluHisTyrValAla... 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 eGlnAlaGlyArgPheHisLeuAspGly.....SerArgGlu.... 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 gIleValAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       760 AGAAGAAGTGCCCGCAGCCTGCAACACCTGTGCCGCCTTGTCATCAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 tLeuGlyAlaPro..... 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 TGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGCTCCCACCCCGGC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          560 TCCTGGCCTTTCCGGATGTGGTCAGCCTTGTGCAGCACTATGTGGCCTCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 CAGAAGGCACGTTCTTAGTACGTGACAGCACGCACCCCAGCTACCTGTTC
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     845 GGCGCATGGCCGACTACCTCCGACAGTACCCCTTCCAGCTC 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 GlnArgArgValArgProLeuGlnGluLeuCysArg......GlnAr 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 710 CTCCACCAGCCACTGCTGTACACCTAAAACTGGTGCAGCCCTTTGTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHisPh 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TTGGGGTTCCATTACGGCCAGCGAGGCCCGACAACACCTGCAGAAGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CYTOKINE INDUCIBLE REGULATORY
FITTLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGACTCCAGCTTCCGTCTGGACTCCAACTGCTTGTCCAGGCCACGCA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roValGlyThrPheLeuValArgAspSerArgGlnArgAsnCysPhePhe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roValLeuArgAspTyrLeuSerSerPheProPheGlnIle 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGGTGGCCGACGTGGAC......TGCCTGCCACTGCCCC 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCTGTCAGTGAAAACCACTCGTGGCCCCACCAATGTACGCATTGAGTA 509
                                                                                                                                                                                                                                                                              94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....AlaproArgArgMe 162
                                                                                                                                                                                                                                                                                                                                               Palo Alto
                                                                                                                                                                                                                                                                                                                         Ç
                                                                                                                                                                                                                                                                                                                                                                       E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..... 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459
```

```
alignment_block:
US-08-962-560A-4 x US-08-918-206-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-918-206-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-918-206-2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ACCCCGTGCCCGCAGCTCGGGCGCGCCGGCAGCCGATCAGTGGGTGACC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2587 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 381 CCCCAGCTCGGGCGACCTGTCTTTGCCGCGGTGACCCTTCTCTCATG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 CGTTTTGGGATTCGCACTGACTTCAAGGAAGGACGCGAACCCTTCTCTGA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 AGCCCCATCCCTTCTCTCTGCCACCATTTCGGACACCCCGCAGGAACT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: BRSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                     101 rPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSerV 118
                                                                                  581 ATGACTGTTAATGAAGCCAAAGAGAAATTAAAAGAGGCACCAGAAGGAAC
                                                                                                                                                                       531 TCTGGCGAAGGCTGCGGGAGCTCGGTCAGACAGGATGGTACTGGGGAAGT 580
                                                                                                                                                                                                                                                          481 CCAGTGGGGGACCGCGGGGTCGGCGGAGGAGCCATCCCGCAGGCGGCGCG 530
                                                                                                                                                                                                                                                                                                                                            431 ACCCTGCGGTGCCTTGAAGCCTCCGGGAATGGCGGGGAAGGGACGCGGAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 GCGGCTGCGAGGCGACTTTGTCATCCGTCCTCCAGGATCTGGGGAGAAAG
                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 ysproAlaValProAlaPro.....AlaProGlyAspThrHisPheArg 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                               68 leThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyPro
                                                                                                                                                                                                                                                                                                                                                                                       58 ThrPheArg.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 oval.....ArgProArgProC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 uProArgArgSerGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAlaAlaGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                        LeuServalHisGlyAlaHisGluArgLeuArgAlaGluProValGlyTh 101
TTTCTTGATTAGAGATAGCTCGCATTCAGACTACCTACTAACAATATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .........ProSer...SerSerSerSerSerSerSerProAlaAlaPr 37
                                                                                                                                                                                                                                                                                              .....SerH1sSerAspTyrArgArgI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : BRSTNOT13
2787140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240.50
1.743
46.154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 299
Gaps: 10
Percent Identity: 27.425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0372
                                                                                                                                                                                                                                                                                                                                                                                         SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                           60
    680
                                                                                       630
                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgnl_6/ptodata/2/ina/5C_COMB.seq:US-08-463-081B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/08463081B Patent No. 5871960 Patent No. 5871960 5837487
                                                                                   TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
                                                                                                                         NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/104,736 FILING DATE: 10-AUG-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/796,066 FILING DATE: 20-NOV-91 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  881 ACCAAACCGCTC...TACACGTCAGCACCATCTCTGCAGCATCTCTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972 TACCAACAAGACTAAAAGATTACTTGGAAGAATATAAATTCCAGGTA 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI STREET: 444 South Flower St. - Suite 1900 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGGACAGGTCCAGAAGCCCCCCGGAACGGCACTGTTCACCTTTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAlaProLeuArgGlnArgArgValArgProLeuGlnGluLeuCysAr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euAsnProValLeuArgAspTyrLeuSerSerPheProPheGlnIle 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCACCATTAACAAATGTACCGGTGCC.....ATCTGGGGACTGCCTT 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACAGTGTGGTTCATCTGATCGACTACTATGTTCAGATGTGCAAGGATA 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATTCAGATTGGACTCTATCATATGTGTCAAATCCAAGCTTAAACAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gGlnArgIleValAlaAlaValGlyArgGluAsnLeuAlaArgIleProL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90071
                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                     US/08/463,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-463-081B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-962-560A-4 x US-08-463-081B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-463-081B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                       181
                                                                                                                                                                                                                                                                              166
                                                                                                                                                                                                                                                                                                                      537
                                                                                                                                                                                                                                                                                                                                                                                                     487 TATGTGGCCTCCTGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                               155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AsnCysPhePheAlaLeuSerValLysMetAlaSerGlyProThrSerI1 127
195 leProLeuAsnProValLeuArgAspTyrLeuSerSerPheProPheGln 211
                                                                                                                                                                                           167
                                                                                                                                                                                                                                  587 CACTGCCTGCTCCACCAGCCACTGCTGCTACACCTAAAACTGGTGCAG
                                                                                                                                                                                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TGGCAGAGGGTACCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 GCCCAAGCCAGTCATGCAGCCCTTGCCTGGGGGCCTTCCTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 rProAlaAlaProValArgProArgProCysProAlaVal...... 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AlaGluProArgArgArgSerGluProSerSerSerSerSerSerSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eArgValHisPheGlnAlaGlyArgPheHisLeuAspGly....... 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euArgAlaGluProValGlyThrPheLeuValArgAspSerArgGlnArg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGAGGAGGATCTGCTGTGCATAGCCAAGACCTTCTCCTACCTTCGGGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGGCCACGCATCCTGGCCTTTCCGGATGTGGTCAGCCTTGTGCAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erArgGlu.....ThrPheAspCysLeuPheGluLeuLeuGluHis 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGTGGAGCGGACTGGGCCAGCGGCCCCTGTGGGCCCCCGTCCCTGGAACT 86
                                                               TGTCATCAACCGTCTGGTGGCCGACGTGGAC......TGCC
                                                                                                                                                 CCCTTTGTACGCAGAAGAAGTGCCCGCAGCCTGCAACACCTGTGCCGCCT 686
                                                                                                                                                                       .....LeuArgGlnArgArgValArgProLeuGlnGluLeuCysArg. 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTACCTGTTCACGCTGTCAGTGAAAACCACTCGTGGCCCCACCAATGT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTGGCTGGTATTGGGGGTTCCATTACGGCCAGCGAGGCCCGACACACC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeuAspAl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......ProAlaProAlaProGlyAspThrHisPheArgThrPheArg
                                                                                                                                                                                                                                                                                                                      TCCCACCCGGCCCTGCCTATGCCTAAGGAGGATGCGCCTAGTGACCCAG
                                                                                                                                                                                                                                                                                                                                                           aProArgArgMetLeuGlyAlaPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrValAla......Al 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCATTGAGTATGCCGACTCCAGCTTCCGTCTGGACTCCAACTGCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......GlnArgIleValAlaAlaValGlyArgGluAsnLeuAlaArgI 195
                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237.00
1.837
51.394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              774
                                                                                                                                                                                                                                                                                                                                                                                                       536
                                                                                                                                                                                                                                    636
                                                                                                                                                                                                                                                                                                                      586
                                                                                                                                                                                                                                                                                                                                                             166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ü
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-461-379A-33
                                                                                                                                                                                                             Align seg 1/1 to: US-08-461-379A-33
                                                                                                                                                                                                                                                    US-08-962-560A-4 x US-08-461-379A-33
                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: G 07/796,066

FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Apparent No. 5871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (610)470-0
TELEFAX: (610)470-070
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 TGCCACTGCCCGGCGCATGGCCGACTACCTCCGACAGTACCCCTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                               87
                                                                                     \frac{3}{3}
                                                                                                                              37
                                                                                                                                                                    17 AlaGluProArgArgArgSerGluProSerSerSerSerSerSerSerSe 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Valley Forge
STATE: Pennsylvani;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release SOFTWARE: Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                            GCTGTGGAGCGGACTGGGCAGCGGCCCCTGTGGGCCCCCGTCCCTGGAACT 86
                                               GCCCAAGCCAGTCATGCAGCCCTTGCCTGCTGGGGGCCTTCCTCGAGGAGG 136
                                                                                   rProAlaAlaProValArgProArgProCysProAlaVal.....
.....ProAlaProAlaProGlyAspThrHisPheArgThrPheArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08461379A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (610)470-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, Kendall A. & Beadling, Carol VENTION: Nucleic Acids Encoding CR5 Polypeptide, VENTION: Vector and Transformed Cell Thereof, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (610)470-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                             237.00
1.837
51.394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/461,379A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33:
                                                                                                                                                                                                                                                                                                                  Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Westlakes-Berwyn
                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                    29.084
                                                                                                                                                                                                               774
                                                                                       46
```

```
seq_documentation_block:
; Sequence 33, Application US/08462390B
                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-462-390B-33
                                                                                                                                                                                                                                                                                            Patent No. 5882894
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155
                                                                                                                                                                    APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CRB Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 leProLeuAsnProValLeuArgAspTyrLeuSerSerPheProPheGln 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 aProArgArgMetLeuGlyAlaPro....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 TGGCAGAGGGTACCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGAC
COMPUTER READABLE FORM
                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 Ile 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 TGCCACTGCCCCGGCGCATGGCCGACTACCTCCGACAGTACCCCTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                               CITY: Valley Forge
STATE: Pennsylvania
                                        COUNTRY:
                                                                                                         ADDRESSEE:
                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erargGlu......ThrPheAspCysLeuPheGluLeuLeuGluHis 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTACCIGTTCACGCTGTCAGTGAAAAACCACTCGTGGCCCCACCAATGT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnCysPhePheAlaLeuSerValLysMetAlaSerGlyProThrSerIl 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgL
                                                                                                                                                                                                                                                                                                                                                                                                                              CTC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCATCAACCGTCTGGTGGCCGACGTGGAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTTTGTACGCAGAAGAAGTGCCCGCAGCCTGCAACACCTGTGCCGCCT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTGCCTGCTCCACCAGCCACTGCTGCTACACCTAAAACTGGTGCAG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGTGGCCTCCTGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrValAla......Al 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGCCACGCATCCTGGCCTTTCCGGATGTGGTCAGCCTTGTGCAGCAC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCATTGAGTATGCCGACTCCAGCTTCCGTCTGGACTCCAACTGCTTGT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eArgValHisPheGlnAlaGlyArgPheHisLeuAspGly...... 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euArgAlaGluProValGlyThrPheLeuValArgAspSerArgGlnArg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTGGCTGGTATTGGGGTTCCATTACGGCCAGCGAGGCCCGACAACACC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGAGGAGGATCTGCTGTGCATAGCCAAGACCTTCTCCTACCTTCGGGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeuAspAl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCACCCGGCCCTGCCTATGCCTAAGGAGGATGCGCCTAGTGACCCAG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......GlnArgIleValAlaAlaValGlyArgGluAsnLeuAlaArgI 195
                                                             Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuArgGlnArgArgValArgProLeuGlnGluLeuCysArg.. 180
                                            USA
                                                                                                                                 Ratner & Prestia
                                                                                                            (B) STREET:One Westlakes-Berwyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....TGCC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..... 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
```

Floppy disk

```
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
TYPE: nucleic single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-462-390B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-962-560A-4 x US-08-462-390B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-462-390B-33 from: 1 to: 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1vlana Amzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
                                                                                          337
                                                                                                                                                                                                                                                                           237 ATCTGGCTGGTATTGGGGTTCCATTACGGCCAGCGAGGCCCGACAACACCC
387 ACGCATTGAGTATGCCGACTCCAGCTTCCGTCTGGACTCCAACTGCTTGT 436
                                                                                                                                                                                 187 CCAGAGGAGCATCTGCTGTGCATAGCCAAGACCTTCTCCTACCTTCGGGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DA TELECOMMUNICATION INFORMATION: TELEPHONE: (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                        94 euArgAlaGluProValGlyThrPheLeuValArgAspSerArgGlnArg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  61 SerHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeuAspAl 77 ::::::||| ::: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 rProAlaAlaProValArgProArgProCysProAlaVal..... 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 AlaGluProArgArgArgSerGluProSerSerSerSerSerSerSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 GCTGTGGAGCGGACTGGGCAGCGGCCCCTGTGGGCCCCGTCCCTGGAACT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/330,108 FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
COMPUTER: II
                        eArgValHisPheGlnAlaGlyArgPheHisLeuAspGly....... 141
                                                                                     aCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAAGCCAGTCATGCAGCCCTTGCCTGCTGGGGCCTTCCTCGAGGAGG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCAGAGGGTACCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......ProAlaProAlaProGlyAspThrHisPheArgThrPheArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237.00
1.837
51.394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 251
Gaps: 7
Percent Identity: 29.084
                                                                                                                                                                                                                                                                           286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
```

CURRENT APPLIC FILING CLASSI ATTORNEY NAME: REGIST REGIST TELECOMM TELLEFA INFORMATIO SEQUENCE LENGTH TYPE: STRAND MOLECULE FEATURE: RAME/K	Seq_documenta; Sequence 1, Sequence 1, GENERAL IN GENERAL IN TITLE OF NUMBER O) CORRESPO) CORRESPO; STREET COUNTR: STATE: COMPUTER COMPUTE	141 437 155 487 158 537 166 587 167 181 687 195 722 212 272
APPLICATION DATA APPLICATION DATA ATION NUMBER: U DATE: 10-JUN-1 FICATION: 435 FICATION: 435 FICATION: 435 FICATION INFORMATI MYCES, COLORET NUMBER: UNICATION INFORMATI NUMCE, (617) 227-59 N TOR SEQ ID NO- N: (617) 227-59 N FOR SEQ ID NO- N: CHARACTERISTICS: CHARACTERISTICS: 5737 base pai nucleic acid EDNESS: single TYPE: CDN EY: CDS	Seq_documentation_block: Sequence 1, Application US/082592 Patent No. 5650293 GENERAL INFORMATION: APPLICANT: White, Morris F. TITLE OF INVENTION: pp60PIX: NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIE STREET: 60 STATE STREET, SU CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: USA ZIP: 02109 COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS	ENAFGLUTIPPER
1: 1994 2994 259, 264 35, 965 35, 965 35, 965 1 JDP-021 RR: JDP-02	259264 EK: A DOWNSTREAM ELEMENT IN (FIELD (SUITE 510) MS-DOS	SPCYSLEUPREGULLEULEULEUS IN SPCYSLEUPREGULLEULEULEUS IN SECTOR SECTOR SECONDATE SECTION OF THE PROPERTY OF THE PROPERTY OF THE SECTION OF THE
	N INSULIN SIGNALING	1

1388..2749

```
seq_documentation_block:
; Sequence 1, Application US/08076011
; Patent No. 5521069
                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-076-011-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-962-560A-4 x US-08-259-264-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-08-259-264-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-259-264-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1615 AGATGGTACCTTCTTAGTTCGTGATGCCTCAACGAAAATGCAGGGGGATT 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1856 CAACAGGATCAGTTGGTAAAAGAAGATAACATTGATGCAGTAGGTAAA 1903
                                                                                                                                                   APPLICANT: KIMURA, Chiharu
APPLICANT: OHKUBO, Shoichi
TITLE OF INVENTION: NOVEL DNA AND USE THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 PheGlnAlaGlyArgPheHisLeuAspGlySerArgGlu.....ThrPh 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 heAlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHis 130
                                                                                                                                                                                                                                                                                       APPLICANT: ONDA, Haruo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 aProGly.....AspThrHisPheArgThrPheArgSerHisSerAspT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 ProAlaAlaProValArgProArgProCysProAlaValProAlaProAl 50
STATE: Massachusetts
COUNTRY: US
                                                                         STREET:
                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     etLeuGlyAlaProLeuArgGlnArgArgValArgProLeu...... 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGCTCTTCCACCAAAGCCA...CCTAAGCCAATGACTCCAGCAGTCAC 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTACAATCCCAAACTCGACGTGAAGCTGACGTACCCAGTATCCAGATTC 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTTCTGTGGTGGAGCTTATTAACCACTACCACCACGAGTCTCTCGCTC 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eAspCysLeuPheGluLeuGluHisTyrValAlaAlaProArgArgM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCGGGATGGTAAATAT......GGCTTCTCTGAGCCCCTGACGTT 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oValGlyThrPheLeuValArgAsp...SerArgGlnArgAsnCysPheP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGGAGATATTTCCAGGGAAGAGGTAAATGACAAATTGCGGGACATGCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TrpGlyProLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluPr 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACATTGACTTTGAGGAAGGGAGGAAATAATAAATTAATAAAGATCTAT 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yrArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyr 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....GlnGluLeuCysArgGlnArgIleValAlaAlaValGlyArg 189
                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                         130 Water Street
                                                                                                     DAVID G. CONLIN; DIKE, BRONSTEIN ROBERTS & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122.50
1.392
53.012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....TCTCTTCAAGATGCA...GAGTGGTAC 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 8
Percent Identity: 27.108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 5737
```

```
NAME/KEY:
; LOCATION:
; LOCATION:
; COCATION:
US-08-076-011-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-962-560A-4 x US-08-076-011-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-076-011-1 from: 1 to: 17041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 4115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17041 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                         6696 GTAGCAGCAGCAGCCGCAGCTTCAGAGGCAGCCGGAGAGACCTCGGA 6745
                                                                                                                                                                                                                                                      6781 GCCCGCGCTCCTACAAAGGCGGGCTAGCCGCCCGCCCTCTCCCTTGCCT
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,011
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/741,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,246
FILING DATE: 13-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                             52 GlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgArgIl 68
                                                                                                                                                                                                                                                                                            35 laAlaProValArgProArgProCysProAlaValProAlaProAlaPro 51
                                                                                                                                                                                                                                                                                                                                                                         18 uProArgArgArgSerGluProSerSerSerSerSerSerSerFroA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAlaAlaGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 07-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                     euSerValHisGlyAlaHisGluArgLeuArgAlaGluProValGly... 100
                                                                                                                         eThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyProL 85
                                                                                                                                                                TCCTCCCCTTCTTTCTGACTTTC......6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESNICK, DAVID S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(7540..7650, 9814..9945, 10421..10519,
11602..11787)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121.00
1.235
43.946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
                                                                        ......CCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
Percent Identity:
.CGCCTGCTTCTTCCTCCGGGTGGACTT 6896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41155-CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223
10
27.803
                                                                                   6858
                                                                                                                                                                                                                                                      6830
                                                                                                                                                                                                                                                                                                                                          6780
```

```
; LENGTH: 2508
; TYPE: DNA
; ORGANISM: human
US-08-850-993-1
                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn1_6/ptodata/2/ina/5D_COMB.seq:US-08-850-993-1
                                                                                                                                                 Align seg 1/1 to: US-08-850-993-1
                                                                                                                                                                                              US-08-962-560A-4 x US-08-850-993-1
                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Hansen, Torben
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Pedersen, Oluf B.

TITLE OF INVENTION: Mutant cDNA Encoding The p85alpha
TITLE OF INVENTION: Subunit Of Phosphatidylinositol 3-Kinase
FILE REFERENCE: 4802.200-05
CURRENT APPLICATION NUMBER: US/08/850,993
CURRENT FILING DATE: 1997-05-05
EARLIER APPLICATION NUMBER: 0539/96
EARLIER FILING DATE: 1996-05-06
NUMBER OF SEC IT NOC. 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08850993 Patent No. 5955277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7170 CCGTCCTACCTGGCAGCTCTCCTGGCAGCGGGAGGAGTTGAAGGGTAAGG 7219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7070 CCCGCTGGTTCCTGCGGCTTCTGCTCAGACACCAACGCCAGACGGCGATG 7119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7029 ACGAGCCTCGGCAAACGA.....GTCCCGCAGCTCCTCCTGCTGCT 7069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
                                             943 CAGCCTGCACCACCACCTCCTAAACCACCAAAACCTACT..... 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 lnAlaGlyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 PheGluLeuLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAl 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                              41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTCTCGGGTGGTGACTCCAGCGCAGGAACTTGAAGAAGCGCTTTGCCCCG 7169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgGlnArgArgValArgProLeuGlnGlu.....LeuCysArg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGGAAAATCTTACCAAA 7238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yArgGluAsnLeuAlaArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTGGTTCTGCGCGTCTA......CAAACTTTTGAGCAGAAC 7028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aLeuSerValLysMetAlaSerGlyProThrSerIleArgValHisPheG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGGCCACCTTGCTCCGCGCGCTTCACCTCATCGCCCCCCTCTTT.... 6941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAl 115
                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                      119.50
1.258
53.073
                                                                                                                                                                                                                                                                   Length: 179
Gaps: 7
Percent Identity: 24.581
                                                                                                                                                 from: 1
                                                                                                                                                 to: 2508
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-07-906-349A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applic Patent No. 5434064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1301 ATGTGAAATTACTTTATCCAGTATCCAAATACCAACAGGATCAAGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1119 GTCTACTAAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1069 AATGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1019 CCTTACAAAATGCTGAATGGTACTGGGGAAGATATCTCGAGGGAAGAAGTG 1068
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1169 ATAACAAATTAATCAAAATA.......TTTCATCGAGAT 1200
FILING DATE: 18-UAN TELECOMMUNICATION INFORMATION: 202-628-5197
                                                                     APPLICATION NUMBER: US/07/906,349A FILING DATE: 30-JUN-1992 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/643,237 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L.
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES
TITLE OF INVENTION: TARGET PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 oLeuAsnProValLeuArgAspTyrLeuSerSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 GlySerArgGlu......ThrPheAspCysLeuPheGluLe 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 lyProThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeuAsp 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 985 ACTGTAGCCAACAACGGT.....ATGAATAACAATATGT 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp.. 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 419 Sever
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....TACATGAATATAACACTCAGTTT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAAATATGGCTTCTCTGACCCATTAACCTTCAGTTCTGTGGTTGAATT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .SerArgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AlaAlaValGlyArgGluAsnLeuAlaArgIlePr 196
                                                                                                                                                                                                                                                                                                                                                                                                     20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/07906349A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Browdy and Neimark
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
```

```
alignment_block:
US-08-962-560A-4 x US-07-906-349A-1
                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                    seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-167-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-906-349A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-07-906-349A-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                              Patent No.
                                                                                                                  Sequence 1,
                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 1354
                                                                                                                                                                                                                                                                                                                                                                                                                         1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1072
                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1172 ATAACAAATTAATCAAAATA..........TTTCATCGAGAT 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1122 GTCTACTAAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022 CCTTACAAAATGCTGAATGGTACTGGGGAGATATCTCGAGGGAAGAGTG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3372 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                   196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            946 CAGCCTGCACCAGCACTGCCTCCTAAACCACCAAAACCTACT...... 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp.. 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr :::|||:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlySerArgGlu......ThrPheAspCysLeuPheGluLe 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 1121
                                                                                                                                                                                                                                                                                oLeuAsnProValLeuArgAspTyrLeuSerSerPhe
                                                                                                                                                                                                                                                                                                                              AAAGAAGATAATTGAAGCTGTAGGGAAAAAA......
                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTGAAATTACTTTATCCAGTATCCAAATACCAACAGGATCAAGTTGTC 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAAATATGGCTTCTCTGACCCATTAACCTTCAGTTCTGTGGTTGAATT 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyProThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeuAsp 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .ACTGTAGCCAACAACGGT......ATGAATAACAATATGT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                                                                                                                                                                    .....TTACATGAATATAACACTCAGTTT 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerArgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerG 123
                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                    Application US/08167035
Schlessinger, Joseph
Skolnick, Edward Y.
Margolis, Benjamin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119.50
1.258
53.073
Edward Y.
Benjamin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 24.581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 3372
                                                                                                                                                                                                                                                                                   208
```

```
alignment_block:
US-08-962-560A-4 x US-08-167-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-167-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-167-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: INVENTION: INVENTION: ITITLE OF SEQUENCES:
                                                                                                                                                                                                                                    1072 AATGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COTUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 768:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 3372 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08 FILING DATE: 16-DEC-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
123 lyProThrSerIleArgValH1sPheGlnAlaGlyArgPheH1sLeuAsp 139
                                                                                                                                                                                                                                                                                                                          988 .ACTGTAGCCAACAACGGT......ATGAATAACAATATGT 1021
                                                                                                                                                                                                                                                                                                                                                                                                             946 CAGCCIGCACCAGCACTGCCTCCTAAACCACCAAAACCTACT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla
                                                                                                                                                                                                                                                                                                                                                                57 gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: 10036-
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                            HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp.. 106
                                                                   GTCTACTAAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 1171
                                                                                                         .SerArgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
)EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
Y: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3372 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
43..2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119.50
1.258
53.073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOVEL EXPRESSION CLONING METHOD FOR IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND NOVEL TARGET PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us/08/167,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 7
Percent Identity: 24.581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7683-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                 987
```

```
seq_name: /cgn1_6/ptodata/2/1na/5A_COMB.seq:US-08-167-035-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1172 ATAACAAATTAATCAAAATA.....TTTCATCGAGAT 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1204 GGGAAATATGGCTTCTCTGACCCATTAACCTTCAGTTCTGTGGTTGAATT
                                                                                   ; MOLECULE TYPE: US-08-167-035-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1254 AATAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1304
                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
Ratio:
percent Similarity:
                                                                                                                                                                                    TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          NAME: COTUZZI, Laura A. REGISTRATION NUMBER: 30,742 REGISTRATION NUMBER: 768 REFERENCE/DOCKET NUMBER: 768 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTGAAATTACTTTATCCAGTATCCAAATACCAACAGGATCAAGTTGTC 1353
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION:
TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTACATGAATATAACACTCAGTTT 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oLeuAsnProValLeuArgAspTyrLeuSerSerPhe 208
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 16-DEC
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDRESSEE:
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITY: New York
                                                                                                                  TOPOLOGY:
                                                                                                                                  STRANDEDNESS:
                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                 ELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....AlaAlaValGlyArgGluAsnLeuAlaArgIlePr 196
                                                                                                                                                                                                                                                                                                                                                                                                                                             10036-2711
                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                      nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margolis, Benjamin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10036-2711
                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                              3372 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ication US/08167035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               essinger, Joseph
                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                16-DEC-1993
       119.50
1.258
53.073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVEL EXPRESSION CLONING METHOD FOR IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND NOVEL TARGET PROTEINS
                                                                                                                                                                                                                    869-9741/8864
                                                                                                                                                                                                                                                                                                                                               US/08/167,035
                                                                                                                                                                                             48:
          Gaps: 7
Percent Identity: 24.581
                                                                                                                                                                                                                                                                  7683-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
```

```
alignment_block:
US-08-962-560A-4 x US-08-167-035-48/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: US-08-167-035-48 from: 1 to: 3372
                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-208-887A-1
                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2427 CAGCCTGCACCAGCACTGCCTCCTAAACCACCAAAACCTACT...... 2386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2385 ACTGTAGCCAACAACGGT.....ATGAATAACAATATGT 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2351 CCTTACAAAATGCTGAATGGTACTGGGGAGATATCTCGAGGGAAGAAGTG 2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2301 BATGAAAACTICGAGATACAGCAGACGGACCTTTTTGGTACGAGATGC 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2251 GTCTACTAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 ArgproCysproAlaValProAlaProAlaProGlyAspThrHisPheAr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2169 GGGAAATATGGCTTCTCTGACCCATTAACCTTCAGTTCTGTGGTTGAATT 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 .SerargGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 euleuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp. 106
                                                                                                                                                                                                                                                                                                                                                                                           1986 ......TTACATGAATATAACACTCAGTTT 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                             196 oLeuAsnProValLeuArgAspTyrLeuSerSerPhe
                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lyproThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeuAsp 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uLeuGluH1sTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
                                                                                                                                                                            TLE OF INVENTION:
TLE OF INVENTION:
TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTGAAATTACTTTATCCAGTATCCAAATACCAACAGGATCAAGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....AlaAlaValGlyArgGluAsnLeuAlaArgIlePr 196
                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                   , Application US/08208887A 5677421
                                                       10036-27
                                                                                    New York
                                                                                                                   E: PENNIE & EDMONDS
                                                                                                                                                                                   Skolnick, Edward V.

Skolnick, Benjamin L.

MARGOLIS, Benjamin L.

MARGOLIS, Benjamin L.

MOVEL EXPRESSION CLONING METHOD FOR
FENTION: IDENTIFYING TARGET PROTEINS
FENTION: KINASES AND NOVEL TARGET PROTEINS
                                                                      10036-2711
                                                                                                                                                                                                                                                                    Schlessinger, Joseph
                                                                                                                            the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2020
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-208-887A-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-962-560A-4 x US-08-208-887A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-208-887A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                 1204 GGGAAATATGGCTTCTCTGACCCATTAACCTTCAGTTCTGTGGTTGAATT 1253
                                                                                                                                                                                                                1172 ATAACAAATTAATCAAAATA...
                                                                                              151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
                                                                                                                                                                                                                                                                    1122 GTCTACTAAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 1171
                                                                254 AATAAACCACTÁCCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1303
                                                                                                                                                                                                                                                                                                                                        1072 AATGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 1121
                                                                                                                                                                140 GlySerArgGlu.....ThrPheAspCysLeuPheGluLe 151
                                                                                                                                                                                                                                  123 lyProThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeuAsp 139
                                                                                                                                                                                                                                                                                                                                                                                                        1022 CCTTACAAAATGCTGAATGGTACTGGGGAGATATCTCGAGGGAAGAAGTG 1071
                                                                                                                                                                                                                                                                                                   107 .SerArgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         988 .ACTGTAGCCAACAACGGT.....ATGAATAACAATATGT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         946 CAGCCTGCACCACCACTGCCTCCTAAACCACCAAAACCTACT..... 987
                                                                                                                                                                                                                                                                                                                                                            91 HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp., 106
                                                                                                                                                                                                                                                                                                                                                                                                                                        74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE NFORMATION FOR SEQ ID NO:
                               rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3372 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
(GTGAAATTACTTTATCCAGTATCCAAATACCAACAGGATCAAGTTGTC 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : ABOTOGA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3372 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43..2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119.50
1.258
53.073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/208,887A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 24.581
                                                                                                                                                                                                     .....TTTCATCGAGAT 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7683-063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 3372
```

```
alignment_block:
US-08-962-560A-4 x US-08-539-005-1
                                                                                                                                                                                                                             ; NAME/KEY: LOCATION: US-08-539-005-1
                                  Align seg 1/1 to: US-08-539-005-1 from: 1 to: 3372
                                                                                                                                                                           alignment_scores:
                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn1_6/ptodata/2/ina/5c_comb.seq:US-08-539-005-1
                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION UNDER: US/08/539,005
ETINING DATE: 4-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/167,035
ETILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: CONTACT TENERS
41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr 57
                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .documentation_block:
                                                                                                                                                                                                                                                                                                            POPOLOGY:
                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1354 AAAGAAGATAATATTGAAGCTGTAGGGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                     felefax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 oLeuAsnProValLeuArgAspTyrLeuSerSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AlaAlaValGlyArgGluAsnLeuAlaArgIlePr 196
                                                                                                                                                                                                                                                                                                                                    nucleic acto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10036-2711
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                  3372 base pairs
                                                                                                                                                                                                                                      CDS
43..2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATGOlis, Benjamin L.
IVENTION: NOVEL EXPRESSION CLONING METHOD FOR IVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE IVENTION: KINASES AND NOVEL TARGET PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlessinger, Joseph
                                                                                                                          119.50
1.258
53.073
                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ication US/08539005
                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                                                                                                                                                                                                                                                                                 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTACATGAATATAACACTCAGTTT 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edward
                                                                                                               Percent Identity: 24.581
                                                                                                                                                                                                                                                                                                                                                                                                                                                               683-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..... 1386
```

